

Name _____

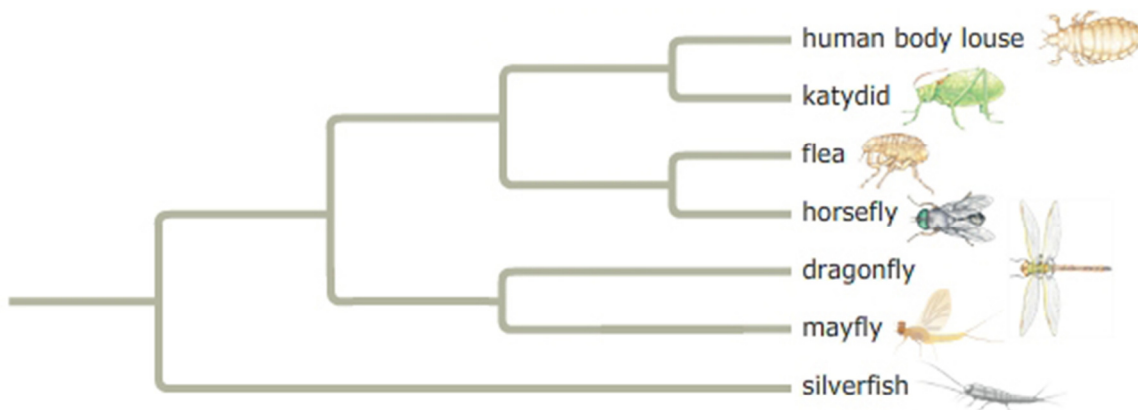
Phylogenetic Trees Practice

Constructing Phylogenetic Trees

A phylogenetic tree is a branching diagram that represents a hypothesis about the evolutionary history of a group of organisms and the relationships between them.

Part A - Reading a phylogenetic tree

This is one possible phylogenetic tree representing the relationships between some members of phylum Arthropoda.



Adapted from *Biology* by Campbell and Reece © Pearson Education, Inc.

Use this phylogenetic tree and your knowledge of cladistics to determine the relationships between these species.

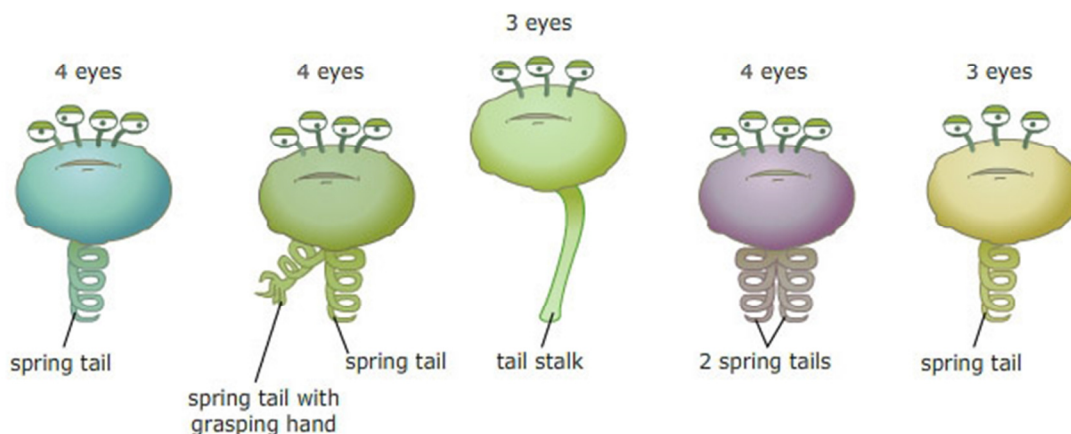
Rank the species from most closely related to horseflies to most distantly related to horseflies. If two species are equally close in their relatedness to horseflies, overlap them.

katydid flea silverfish mayfly human body louse dragonfly

most closely related to horseflies	most distantly related to horseflies

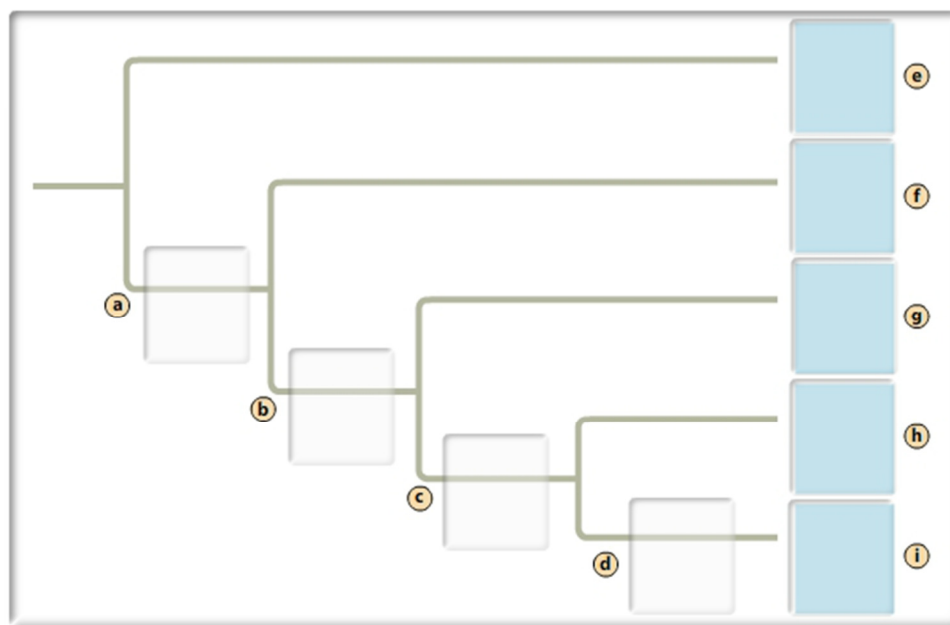
Part B - Constructing a hypothetical phylogenetic tree based on morphology

Imagine that you are studying alien life-forms discovered on a distant planet. While geneticists are working out the genetic code of these organisms, you are asked to construct a phylogenetic tree based on four morphological features, or *characters*: presence or absence of a spring tail, presence or absence of a grasping hand, presence or absence of a second tail, and number of eyes. The organisms have been divided into five groups based on these characters.

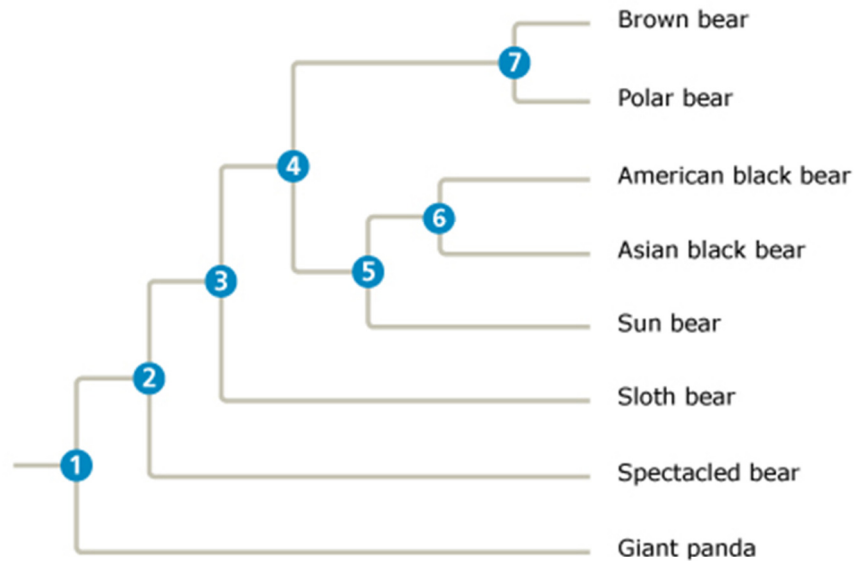


If we assume the alien with a tail stalk is an outgroup, what is the most likely phylogenetic tree based on these shared derived characters? When did these characters appear during the aliens' evolutionary history?

Cut out and paste the aliens and shared derived characters in their appropriate locations on this phylogenetic tree. Use only the blue labels for the blue targets and the white labels for the white targets.



Scientific Skills Exercise: Interpreting Data in a Phylogenetic Tree



Data from J. Krause et al., Mitochondrial genomes reveal an explosive radiation of extinct and extant bears near the Miocene-Pliocene boundary, *BMC Evolutionary Biology* 8: 220 (2008).

What are the evolutionary relationships among bears?

Researchers have long debated different hypotheses for the phylogeny and classification of species in the bear family, Ursidae. In 2008, researchers obtained complete mitochondrial DNA (mtDNA) genome sequences for the eight living species of bears. Based on these data, the researchers constructed a phylogenetic tree for the family Ursidae.

For each of the following questions, circle the correct answer.

Part A - Interpreting the phylogenetic tree

Which branch point represents the most recent common ancestor of all bears?

- ☐ branch point 1
- ☐ branch point 2
- ☐ branch point 3
- ☐ The most recent common ancestor to all living bears is not shown in this tree.

Part B

Which branch point represents the most recent common ancestor of the sloth bear and the spectacled bear?

- ☐ branch point 1
- ☐ branch point 2
- ☐ branch point 3
- ☐ The sloth bear and the spectacled bear do not share a common ancestor.

Part C

Which branch point represents the most recent common ancestor of the Asian black bear and the brown bear?

- ☐ branch point 2
- ☐ branch point 3
- ☐ branch point 4
- ☐ branch point 5

Part D

Which species is the basal taxon in this tree?

- ☐ the spectacled bear
- ☐ the polar bear
- ☐ the sloth bear
- ☐ the giant panda

Part E

Identify the sister taxon to the polar bear.

- ☐ the brown bear
- ☐ the Asian black bear
- ☐ the American black bear
- ☐ the ancestor represented by branch point 7

Part F

According to this tree, is the sun bear more closely related to the sloth bear or the polar bear?

- ☐ the polar bear
- ☐ the sloth bear
- ☐ The sloth bear and the polar bear are equally distant relatives of the sun bear.

Part G - Modifying the phylogenetic tree based on different data

A study published in 2000 sequenced part of the mitochondrial cytochrome *b* gene from 61 brown bears from two sites in Alaska. One population of brown bears lives on the coastal mainland of Alaska, while a separate population lives on the ABC islands in southeastern Alaska.

Mainland and ABC brown bears differ by 11 fixed nucleotide substitutions in the cytochrome *b* gene. This suggests that the two brown bear populations represent genetically unique clades.

The researchers compared the cytochrome *b* sequences of the two clades of Alaskan brown bears to those of 55 polar bears. The analysis showed that polar bears and ABC brown bears differ at only three nucleotides in this gene, whereas polar bears and mainland brown bears had more differences.

Based on the results of the 2000 study, how should the portion of the tree extending from branch point 7 be altered?

